



X16760-pkd.ST25.txt
SEQUENCE LISTING

<110> Allan, Barrett W.
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Marquis, David M.
Ondek, Brian
Watkins, Jeffry D.

<120> CD20 BINDING MOLECULES

<130> AME-09016

<140> 10/849,615
<141> 2004-05-20

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<170> PatentIn version 3.3

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20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
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Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Leu Ser Asn Pro Pro Thr
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Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
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caggctccca ggctcctcat ctatgccaca tccgctctgg cttctggcat cccagacagg 180

ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa 240

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 20 25 30

Asn Met His Trp val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Ala Ile Tyr Pro Leu Thr Gly Asp Thr Ser Tyr Asn Gln Lys Ser
 50 55 60

Lys Leu Gln val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

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Lys Gly Thr Thr val Thr val Ser Ser
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20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
35 40 45

Ala Thr Ser Gly Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
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Asp Val Ala Thr Tyr Tyr Cys Gln Thr Trp Thr Phe Asn Pro Pro Thr
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Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
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aaagttccta agctcttgat ctatgccaca tccggcctgg cttctggggg cccatctcgg 180
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Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60
Lys Trp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Gln Phe Asp Glu Trp Gly
100 105 110

Lys Gly Thr Thr Val Thr Val Ser Ser
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cctggacaag ggcttgagtg gatgggagcc atctatcctg gaaatgggtga tacaagctac 180
aatcagaagt ttaaattggag agtcaccatg accagggaca cgtccacgag cacagtctac 240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagatcgact 300
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<210> 67
<211> 213
<212> PRT
<213> artificial

<220>
<223> synthetic construct

<220>
<221> MISC_FEATURE
<222> (1)..(213)
<223> AME 33 complete light chain

<400> 67

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Pro Tyr Ile
20 25 30

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His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Ala Thr Ser Ala Leu Ala Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Trp Leu Ser Asn Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 68
<211> 642
<212> DNA
<213> artificial

<220>
<223> synthetic construct

<220>
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<222> (1)..(642)
<223> AME 33 complete light chain
<400> 68

x16760-pkd.ST25.txt

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ctctcctgca gggccagctc aagtgtaccg tacatccact ggtaccagca gaaacctggc 120
caggctccca ggctcctcat ctatgccaca tccgctctgg cttctggcat cccagacagg 180
ttcagtggca gtgggtctgg gacagacttc actctcacca tcagcagact ggagcctgaa 240
gattttgcag tgtattactg tcagcagtgg ctgagtaacc caccacttt tggccagggg 300
accaagctgg agatcaaacg aactgtggct gcaccatctg tcttcattct cccgccatct 360
gatgagcagt tgaaatctgg aactgcctct gttgtgtgcc tgctgaataa cttctatccc 420
agagaggcca aagtacagtg gaagggtgat aacgccctcc aatcgggtaa ctcccaggag 480
agtgtcacag agcaggacag caaggacagc acctacagcc tcagcagcac cctgacgctg 540
agcaaagcag actacgagaa acacaaagtc tacgcctgcg aagtcaccca tcagggcctg 600
agctcgcccc tcacaaagag cttcaacagg ggagagtgtt ag 642

<210> 69
<211> 451
<212> PRT
<213> artificial

<220>
<223> Synthetic construct

<220>
<221> MISC_FEATURE
<222> (1)..(451)
<223> AME 33 complete heavy chain

<400> 69

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Arg Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ala Ile Tyr Pro Leu Thr Gly Asp Thr Ser Tyr Asn Gln Lys Ser
50 55 60

Lys Leu Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Ser Thr Tyr Val Gly Gly Asp Trp Gln Phe Asp Val Trp Gly

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360

355

365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 70
<211> 1356
<212> DNA
<213> artificial

<220>
<223> Synthetic construct

<220>
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<222> (1)..(1356)
<223> AME 33 complete heavy chain

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cccgggaaag gcctggagtg gatgggggct atttatccct tgacgggtga tacttcctac 180
aatcagaagt cgaaactcca ggtcaccatc tcagccgaca agtccatcag caccgcctac 240
ctgcagtgga gcagcctgaa ggcctcggac accgccatgt attactgtgc gagatcgact 300
tacgtgggag gtgactggca gttcgaatgc tggggcaagg ggaccacggt caccgtctcc 360
tcagcctcca ccaagggccc atcgggtcttc cccctggcac cctcctccaa gagcacctct 420
gggggcacag cggccctggg ctgcctggtc aaggactact tccccgaacc ggtgacggtg 480
tcgtggaact caggcgccct gaccagcggc gtgcacacct tcccggtgt cctacagtcc 540
tcaggactct actccctcag cagcgtggtg accgtgccct ccagcagctt gggcaccag 600
acctacatct gcaacgtgaa tcacaagccc agcaacacca aggtggacaa gaaggttgag 660

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cccaaattctt gtgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg 720
ggaccgtcag tcttctcttt ccccccaaaa cccaaggaca ccctcatgat ctcccggacc 780
cctgaggtca catgctgtgt ggtggacgtg agccacgaag accctgaggt caagttcaac 840
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aacagcacgt accgtgtgtgt cagcgtcttc accgtcctgc accaggactg gctgaatggc 960
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gagctgacca agaaccaggt cagcctgacc tgcctggtca aaggcttcta tcccagcgac 1140
atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc 1200
gtgctggact ccgacggctc cttcttcttc tatagcaagc tcaccgtgga caagagcagg 1260
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<210> 71
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<213> Homo sapiens

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<220>
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<223> FRL1 VKIII (A27)(DPK22)

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<400> 71

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
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Glu Arg Ala Thr Leu Ser Cys
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<210> 72
<211> 15
<212> PRT
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<220>
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<223> FRL2 VKIII (A27)(DPK22)

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<400> 72

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 73

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<211> 32
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(32)
<223> FRL3 VkiIII (A27)(DPK22)

<400> 73

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 74
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> FRL4 VkiIII (A27)(DPK22)

<400> 74

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 75
<211> 69
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> FRL1 VkiIII (A27)(DPK22)

<400> 75
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ctctcctgc 69

<210> 76
<211> 45
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> FRL2 VkiIII (A27)(DPK22)

x16760-pkd.ST25.txt

<400> 76
tggtaccagc agaaacctgg ccaggctccc aggctcctca tctat 45

<210> 77
<211> 96
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(96)
<223> FRL3 vkIII (A27)(DPK22)

<400> 77
ggcatccagc acaggttcag tggcagtggg tctgggacag acttcactct caccatcagc 60
agactggagc ctgaagattt tgcagtgtat tactgt 96

<210> 78
<211> 30
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(30)
<223> FRL4 vkIII (A27)(DPK22)

<400> 78
tttggccagg ggaccaagct ggagatcaaa 30

<210> 79
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> FRH1 VH5-51 (DPK-73)

<400> 79
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15
Ser Leu Lys Ile Ser Cys Lys Gly Ser
20 25

<210> 80
<211> 14
<212> PRT
<213> Homo sapiens

x16760-pkd.ST25.txt

<220>
 <221> MISC_FEATURE
 <222> (1)..(14)
 <223> FRH2 VH5-51 (DP-73)

<400> 80

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
 1 5 10

<210> 81
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> FRH3 VH5-51 (DP-73)

<400> 81

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
 1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 20 25 30

<210> 82
 <211> 11
 <212> PRT
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<220>
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 <222> (1)..(11)
 <223> FRH4 VH5-51 (DP-73)

<400> 82

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
 1 5 10

<210> 83
 <211> 75
 <212> DNA
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<220>
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 <223> FRH1 VH5-51 (DP-73)

<400> 83
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 tcctgtaagg gttct 75

x16760-pkd.ST25.txt

<210> 84
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 <212> DNA
 <213> Homo sapiens

<220>
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 <223> FRH2 VH5-51 (DP-73)

<400> 84
 tgggtgcgcc agatgcccg gaaaggcctg gagtggatgg ggcaggcac catctcagcc 60
 gacaagtcca tcagcaccgc ctacctgcag tggagc 96

<210> 85
 <211> 42
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(42)
 <223> FRH3 VH5-51 (DP-73)

<400> 85
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<210> 86
 <211> 33
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(33)
 <223> FRH4 VH5-51 (DP-73)

<400> 86
 tggggcaagg ggaccacggt caccgtctcc tca 33

<210> 87
 <211> 23
 <212> PRT
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<220>
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 <223> FRL1 VKI (DPK4)(A20)

<400> 87

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

x16760-pkd.ST25.txt

Asp Arg Val Thr Ile Thr Cys
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<210> 88
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(15)
<223> FRL2 VKI (DPK4)(A20)

<400> 88

Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 89
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(32)
<223> FRL3 VKI (DPK4)(A20)

<400> 89

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
20 25 30

<210> 90
<211> 10
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> FRL4 VKI (DPK4)(A20)

<400> 90

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 91
<211> 69
<212> DNA

<213> Homo sapiens

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<222> (1)..(69)

<223> FRL1 vki (DPK4)(A20)

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atcacttgc 69

<210> 92

<211> 45

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<222> (1)..(45)

<223> FRL2 vki (DPK4)(A20)

<400> 92

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<210> 93

<211> 96

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

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<223> FRL3 vki (DPK4)(A20)

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agcctgcagc ctgaagatgt tgccacttat tactgc 96

<210> 94

<211> 30

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(30)

<223> FRL4 vki (DPK4)(A20)

<400> 94

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<210> 95

<211> 25

<212> PRT

<213> Homo sapiens

<220>
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 <222> (1)..(25)
 <223> FRH1 VKI (DP7/21-2)

<400> 95

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
 20 25

<210> 96
 <211> 14
 <212> PRT
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<220>
 <221> MISC_FEATURE
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 <223> FRH2 VKI (DP7/21-2)

<400> 96

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
 1 5 10

<210> 97
 <211> 32
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> FRH3 VKI (DP7/21-2)

<400> 97

Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu
 1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
 20 25 30

<210> 98
 <211> 11
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MISC_FEATURE

x16760-pkd.ST25.txt

<222> (1)..(11)
<223> FRH4 vki (DP7/21-2)

<400> 98

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 99
<211> 75
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(75)
<223> FRH1 vki (DP7/21-2)

<400> 99
cagggtgcagc tgggtgcagtc tgggtgctgaa gtgaagaagc ctggggcctc agtgaaggtg 60
tcctgcaagg catct 75

<210> 100
<211> 40
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(40)
<223> FRH2 vki (DP7/21-2)

<400> 100
ggtgcgacag gcccctggac aagggcttga gtggatggga 40

<210> 101
<211> 96
<212> DNA
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<220>
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<222> (1)..(96)
<223> FRH3 vki (DP7/21-2)

<400> 101
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agatctgagg acacggccgt gtattactgt gcgaga 96

<210> 102
<211> 33
<212> DNA
<213> Homo sapiens

x16760-pkd.ST25.txt

<220>

<221> misc_feature

<222> (1)..(33)

<223> FRH4 Vki (DP7/21-2)

<400> 102

tggggcaaag ggaccacggt caccgtctcc tca

33